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 ASAKURA, MASAHIRO

<120> CYTOLETHAL DISTENDING TOXINS AND DETECTION OF
 CAMPYLOBACTER BACTERIA USING THE SAME AS A TARGET

<130> SHIM-018

<150> JP 2003-408103

<151> 2003-12-05

<160> 79

<170> PatentIn version 3.1

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Phe	Leu	Ala	Cys	Ser	Ser	Lys	Glu	Gln	Gln	Ile	Asn	Pro	Leu	Gly	Arg	
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tct	tac	ggt	aaa	ttt	aac	gat	aac	gat	cct	tta	aaa	ctt	ggt	tca	aaa	144
Ser	Tyr	Gly	Lys	Phe	Asn	Asp	Asn	Asp	Pro	Leu	Lys	Leu	Gly	Ser	Lys	
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cct	aca	ccc	cct	gtc	aaa	caa	aaa	aca	cca	agc	ttg	gta	gaa	ggt	aaa	192
Pro	Thr	Pro	Pro	Val	Lys	Gln	Lys	Thr	Pro	Ser	Leu	Val	Glu	Gly	Lys	
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Lys	Phe	Pro	Ala	Ile	Pro	Leu	Val	Pro	Pro	Val	Ile	Thr	Pro	Asn	Thr	
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Phe	Lys	Gly	Asp	Asn	Ala	Val	Lys	Gly	Pro	Leu	Pro	Arg	Leu	Lys	Ser	
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cca aac gaa ttt gct tca aat gct tta tac gaa aac aca ggt atg gta Pro Asn Glu Phe Ala Ser Asn Ala Leu Tyr Glu Asn Thr Gly Met Val 100 105 110	336
agt gat ttt gtc act att atg aat cct aat gga gca tct tta aca atc Ser Asp Phe Val Thr Ile Met Asn Pro Asn Gly Ala Ser Leu Thr Ile 115 120 125	384
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aac aat aca gta atg att aaa aat gca aaa aca ttt act tgc tta aac Asn Asn Thr Val Met Ile Lys Asn Ala Lys Thr Phe Thr Cys Leu Asn 165 170 175	528
gcc tat aga aat ggc atc gtt cat tat cct tgt gat caa aca aat ttt Ala Tyr Arg Asn Gly Ile Val His Tyr Pro Cys Asp Gln Thr Asn Phe 180 185 190	576
gcg cag ttt tgg aga ctt tat ccg atg act aat gga gct tat caa att Ala Gln Phe Trp Arg Leu Tyr Pro Met Thr Asn Gly Ala Tyr Gln Ile 195 200 205	624
caa aat ttt gcc acc caa caa tgt ata caa aca cct gtt tca aat gta Gln Asn Phe Ala Thr Gln Gln Cys Ile Gln Thr Pro Val Ser Asn Val 210 215 220	672
atg gaa gaa ttt aat ttg agc ttt tat aat att tat tta acc gat tgt Met Glu Glu Phe Asn Leu Ser Phe Tyr Asn Ile Tyr Leu Thr Asp Cys 225 230 235 240	720
ttg aaa gaa aaa gaa aag aat ttg gat aga cag tgg tat ata ggc gct Leu Lys Glu Lys Glu Lys Asn Leu Asp Arg Gln Trp Tyr Ile Gly Ala 245 250 255	768
cct att taa ttttttcgct atgaaaggaa gata atg aaa aaa ata gta ttt Pro Ile Met Lys Lys Ile Val Phe 260	819
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Phe	Asn	Ile	His	Ala	Leu	Ala	Ser	Gly	Gly	Asn	Asp	Ala	Gly	Ala	Ile		
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Val	Ala	Ala	Val	Asp	Met	Phe	Phe	Arg	Asn	Arg	Pro	Asp	Ile	Asn	Trp		
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Leu	Asp	Pro	Asp	Leu	Arg	Ala	Arg	Thr	Arg	Val	Val	Val	Pro	Pro	Ser		
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Ala	Leu	Glu	Gly	Leu	Arg	Thr	Phe	Leu	Ala	Ser	Asp	His	Phe	Pro	Val		
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Asn	Phe	Arg	Arg	Pro			Met	Lys	Lys	Phe	Phe	Ile	Leu	Phe			
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Ser Leu Ser Pro Phe Arg Lys Thr Ser Lys Arg Leu Glu Asp Gln Asn	
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Trp Phe Leu Lys Glu Ile Val Ala Asn Asp Glu Leu Lys Ala Arg Asp	
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Met His Ala Lys Asp Leu Pro Phe Gly Tyr Val Gln Phe Ile Ser Pro	
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Arg Gly Asp Asp Ile Cys Leu Ala Val Leu Ser Glu Lys Ser Phe Gly	
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acc aaa tct tgc aaa caa gat ttg caa gat gga aca atg cag act att	1974
Thr Lys Ser Cys Lys Gln Asp Leu Gln Asp Gly Thr Met Gln Thr Ile	
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Phe Ser Ile Ile Pro Met Thr Asn Gly Ser Ile Gln Ile Arg Ser Leu	
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acc aat ggt ggc aat caa tgc atg agc act ttt cct gac tct agt atc	2070
Thr Asn Gly Gly Asn Gln Cys Met Ser Thr Phe Pro Asp Ser Ser Ile	
	665 670 675
gcc ata gaa aat cgc ttt ggt tta gga gaa tgc ctt ttg gat cgt tct	2118
Ala Ile Glu Asn Arg Phe Gly Leu Gly Glu Cys Leu Leu Asp Arg Ser	
	680 685 690
atc gta act gta tta agc aaa ctt ttc ttt ttc tcc cct gct ata atc	2166
Ile Val Thr Val Leu Ser Lys Leu Phe Phe Phe Ser Pro Ala Ile Ile	
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gaa gca agc gca att tac taa cacttttcta acaaaaccaa gctt	2211
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 Ser Tyr Gly Lys Phe Asn Asp Asn Asp Pro Leu Lys Leu Gly Ser Lys
 35 40 45

Pro Thr Pro Pro Val Lys Gln Lys Thr Pro Ser Leu Val Glu Gly Lys
 50 55 60
 Lys Phe Pro Ala Ile Pro Leu Val Pro Pro Val Ile Thr Pro Asn Thr
 65 70 75 80
 Phe Lys Gly Asp Asn Ala Val Lys Gly Pro Leu Pro Arg Leu Lys Ser
 85 90 95
 Pro Asn Glu Phe Ala Ser Asn Ala Leu Tyr Glu Asn Thr Gly Met Val
 100 105 110
 Ser Asp Phe Val Thr Ile Met Asn Pro Asn Gly Ala Ser Leu Thr Ile
 115 120 125
 Trp Ala Leu Asn Pro Gly Asn Trp Ile Trp Gly Tyr Ser Leu Phe Ala
 130 135 140
 Ser Arg Pro Phe Gly Asp Ala Arg Ala Trp Gln Leu Ile Glu Phe Pro
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 Asn Asn Thr Val Met Ile Lys Asn Ala Lys Thr Phe Thr Cys Leu Asn
 165 170 175
 Ala Tyr Arg Asn Gly Ile Val His Tyr Pro Cys Asp Gln Thr Asn Phe
 180 185 190
 Ala Gln Phe Trp Arg Leu Tyr Pro Met Thr Asn Gly Ala Tyr Gln Ile
 195 200 205
 Gln Asn Phe Ala Thr Gln Gln Cys Ile Gln Thr Pro Val Ser Asn Val
 210 215 220
 Met Glu Glu Phe Asn Leu Ser Phe Tyr Asn Ile Tyr Leu Thr Asp Cys
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 Ala Ala Thr Glu Ser Lys Trp Asn Val Ser Ile Arg Gln Leu Ile Thr
 35 40 45
 Gly Ala Asn Pro Met Asp Val Leu Ala Val Gln Glu Ala Gly Val Leu

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Gly Ile Pro Ile His Glu Tyr Ile Trp Asn Leu Gly Ser Val Ser Arg		
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Pro Ser Ser Val Tyr Ile Tyr Tyr Ser Arg Val Asp Val Gly Ala Asn		
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Arg Val Asn Leu Ala Ile Val Ser Arg Val Gln Ala Asp Glu Val Phe		
	115	120 125
Val Leu Pro Pro Pro Thr Val Ala Ser Arg Pro Ile Ile Gly Ile Arg		
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Ile Gly Asn Asp Ala Phe Phe Asn Ile His Ala Leu Ala Ser Gly Gly		
145	150	155 160
Asn Asp Ala Gly Ala Ile Val Ala Ala Val Asp Met Phe Phe Arg Asn		
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Arg Pro Asp Ile Asn Trp Met Ile Leu Gly Asp Phe Asn Arg Glu Ser		
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Gly Ala Leu Val Thr Leu Leu Asp Pro Asp Leu Arg Ala Arg Thr Arg		
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Val Val Val Pro Pro Ser Ser Thr Gln Thr Ser Gly Arg Thr Ile Asp		
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Tyr Ala Ile Thr Gly Asn Ser Asn Thr Ala Ala Leu Tyr Asn Pro Pro		
225	230	235 240
Pro Ile Val Ala Ile Leu Ala Leu Glu Gly Leu Arg Thr Phe Leu Ala		
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Ile Arg Ser Leu Glu Thr Gly Ile Ser Leu Ser Pro Phe Arg Lys Thr
35 40 45
Ser Lys Arg Leu Glu Asp Gln Asn Trp Phe Leu Lys Glu Ile Val Ala
50 55 60

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Gly	Tyr	Val	Gln	Phe	Ile	Ser	Pro	Arg	Gly	Asp	Asp	Ile	Cys	Leu	Ala
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Val	Leu	Ser	Glu	Lys	Ser	Phe	Gly	Thr	Lys	Ser	Cys	Lys	Gln	Asp	Leu
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Gln	Asp	Gly	Thr	Met	Gln	Thr	Ile	Phe	Ser	Ile	Ile	Pro	Met	Thr	Asn
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Gly	Ser	Ile	Gln	Ile	Arg	Ser	Leu	Thr	Asn	Gly	Gly	Asn	Gln	Cys	Met
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Gly	Glu	Cys	Leu	Leu	Asp	Arg	Ser	Ile	Val	Thr	Val	Leu	Ser	Lys	Leu
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 <400> 39
 aaatttacct caaacgctc ttc 23

<210> 40
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 <212> DNA
 <213> Artificial

 <220>
 <223> an artificially synthesized primer sequence

 <400> 40
 aagcataaat caaggcgacg atc 23

<210> 41
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 <213> Artificial

 <220>
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 <400> 41
 gtatatctag accgttccaa 20

<210> 42
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 aaatcatcat cttgccgcct 20

<210> 43
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 ggaactcttg gattagaaac tc 22

<210> 44
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 <400> 44
 gcgtcagagt aacgttttta aca 23

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<212> DNA
<213> Artificial

<220>
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<400> 45
agccggcgat cttgtccgaa c

21

<210> 46
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<213> Artificial

<220>
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<400> 46
gcaaacctgc ggactcacct a

21

<210> 47
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<212> DNA
<213> Artificial

<220>
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<400> 47
ccacagaaag caaatgga

18

<210> 48
<211> 26
<212> DNA
<213> Artificial

<220>
<223> an artificially synthesized primer sequence

<400> 48
ctaactgtgt aaatttagct atagtt

26

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<212> DNA
<213> Artificial

<220>
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<400> 49
tttttcaata tccatgcttt agc

23

<210> 50
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<220>
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<400> 50
 tggatgatag caggggattt taa

23

<210> 51
 <211> 2180
 <212> DNA
 <213> Campylobacter fetus

<220>
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<220>
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 Met Thr Lys Ile Ile Phe Lys His Ile Lys Asn Ser Leu Ile Leu Leu
 1 5 10 15
 ttt tgt atc gct ctt ttt agt gct tgc tca tca aaa acg aca aat gta 96
 Phe Cys Ile Ala Leu Phe Ser Ala Cys Ser Ser Lys Thr Thr Asn Val
 20 25 30
 agc act caa aaa ata aat cca tta gga agc att ttt ggc aaa acg gat 144
 Ser Thr Gln Lys Ile Asn Pro Leu Gly Ser Ile Phe Gly Lys Thr Asp
 35 40 45
 gat cca gat cca cta aat tta ggc gat ttt cca act ctt cta aca tca 192
 Asp Pro Asp Pro Leu Asn Leu Gly Asp Phe Pro Thr Leu Leu Thr Ser
 50 55 60
 aat ttt aca aat cct atg ccg act aga acg cca tcg cca ctt aaa aaa 240
 Asn Phe Thr Asn Pro Met Pro Thr Arg Thr Pro Ser Pro Leu Lys Lys
 65 70 75 80
 gtg gat ttg cct gta atg aac tca tta aca cat ggt ccg atg ttt tca 288
 Val Asp Leu Pro Val Met Asn Ser Leu Thr His Gly Pro Met Phe Ser
 85 90 95

agt gct ttt agt aaa ccg gac ttg aat ttc aaa caa cct act atc agt Ser Ala Phe Ser Lys Pro Asp Leu Asn Phe Lys Gln Pro Thr Ile Ser 100 105 110	336
cta caa ggt atc ccg cct gat cta ttt gat aga aca agc gat ttt atg Leu Gln Gly Ile Pro Pro Asp Leu Phe Asp Arg Thr Ser Asp Phe Met 115 120 125	384
gtg ata atg ggt gca aac ggc gtt gtg atc act att tgg tac aca tct Val Ile Met Gly Ala Asn Gly Val Val Ile Thr Ile Trp Tyr Thr Ser 130 135 140	432
cct gga aac tgg tta tgg ggc tac tcg ctc tat gaa agc ggc aat tta Pro Gly Asn Trp Leu Trp Gly Tyr Ser Leu Tyr Glu Ser Gly Asn Leu 145 150 155 160	480
gga gga tat cgt gtt tgg cgt cta att tta cta cca aat aat gaa gtc Gly Gly Tyr Arg Val Trp Arg Leu Ile Leu Leu Pro Asn Asn Glu Val 165 170 175	528
atg ata gta aat ttc aac act cgc acg act tgc ata aat act tat aaa Met Ile Val Asn Phe Asn Thr Arg Thr Thr Cys Ile Asn Thr Tyr Lys 180 185 190	576
aac gga gta att cac tca cct tgc aat aaa gat aat cct ttt cag aaa Asn Gly Val Ile His Ser Pro Cys Asn Lys Asp Asn Pro Phe Gln Lys 195 200 205	624
ttt acg ttt cgt cca atg aca aac gga gcc gta caa att tat aac aaa Phe Thr Phe Arg Pro Met Thr Asn Gly Ala Val Gln Ile Tyr Asn Lys 210 215 220	672
gct act aat tgc gtg ctt gca aac gcc tgt taataatcta ttcggttttg Ala Thr Asn Cys Val Leu Ala Asn Ala Cys 225 230	722
acgttttttg ggcgataaat cttacgacaa aatgcactga tactatcgat caaca atg Met 235	780
gta ttt gct ccc gcc gcc gca agt tgg aag act att tta tta gga gta Val Phe Ala Pro Ala Ala Ala Ser Trp Lys Thr Ile Leu Leu Gly Val 240 245 250	828
aaa atg cga aat gtt att atg att ata ttt ata gca act tta ggc ttt Lys Met Arg Asn Val Ile Met Ile Ile Phe Ile Ala Thr Leu Gly Phe 255 260 265	876
gca aaa cca gaa gat tat aaa att gct act tgg aat ttg caa ggc agt Ala Lys Pro Glu Asp Tyr Lys Ile Ala Thr Trp Asn Leu Gln Gly Ser 270 275 280	924
tcg gct ata acc gaa agc aaa tgg aat ata agc gta cgt caa ata att Ser Ala Ile Thr Glu Ser Lys Trp Asn Ile Ser Val Arg Gln Ile Ile 285 290 295	972
agc ggt gaa aat cca gca gat ata tta gcc gtt caa gaa gca gga aat Ser Gly Glu Asn Pro Ala Asp Ile Leu Ala Val Gln Glu Ala Gly Asn 1020	

300	305	310	315	
tta cct caa acc gct ctt cct aca ggt aga agc ata aat caa ggc ggc				1068
Leu Pro Gln Thr Ala Leu Pro Thr Gly Arg Ser Ile Asn Gln Gly Gly	320	325	330	
acg atc gta act gag cat tta tgg cag cta ggc agt ata tct aga ccg				1116
Thr Ile Val Thr Glu His Leu Trp Gln Leu Gly Ser Ile Ser Arg Pro	335	340	345	
ttc caa gtc tat ata tat tat gct caa atc gac aca ggg gca aat aga				1164
Phe Gln Val Tyr Ile Tyr Tyr Ala Gln Ile Asp Thr Gly Ala Asn Arg	350	355	360	
gta aat tta gca atc gtt tca cgc ata aaa gct gat gaa atc atc atc				1212
Val Asn Leu Ala Ile Val Ser Arg Ile Lys Ala Asp Glu Ile Ile Ile	365	370	375	
ttg ccg cct cct acg gta gct tct cgt ccg ctc ata ggt ata aga ata				1260
Leu Pro Pro Pro Thr Val Ala Ser Arg Pro Leu Ile Gly Ile Arg Ile	380	385	390	395
gga aac gac gta ttt ttc aac ata cac gct cta gca aat ggc gga gtc				1308
Gly Asn Asp Val Phe Phe Asn Ile His Ala Leu Ala Asn Gly Gly Val	400	405	410	
gat gct ccg gcg ata ata aat tca ata ttt gac aga ttt aga aat atg				1356
Asp Ala Pro Ala Ile Ile Asn Ser Ile Phe Asp Arg Phe Arg Asn Met	415	420	425	
cca aat atc act tgg atg att tta ggc gat ttt aac cgc tca cct gag				1404
Pro Asn Ile Thr Trp Met Ile Leu Gly Asp Phe Asn Arg Ser Pro Glu	430	435	440	
agt tta aga gga act ctt gga tta gaa act cgc gtc aga gta acg ttt				1452
Ser Leu Arg Gly Thr Leu Gly Leu Glu Thr Arg Val Arg Val Thr Phe	445	450	455	
tta aca cct ccg gcg cct act caa aga agc ggc gga acg ctt gac tgg				1500
Leu Thr Pro Pro Ala Pro Thr Gln Arg Ser Gly Gly Thr Leu Asp Trp	460	465	470	475
gct ata gtt gga aac tca gcc ggc gat ctt gtc cga act acg ctt gta				1548
Ala Ile Val Gly Asn Ser Ala Gly Asp Leu Val Arg Thr Thr Leu Val	480	485	490	
gca gta ttg atg cta gca aac ctg cgg act cac cta gtt tcg gac cat				1596
Ala Val Leu Met Leu Ala Asn Leu Arg Thr His Leu Val Ser Asp His	495	500	505	
ttt ccg gta aat ttt aga aaa ttt gga gat aac ta atg aaa gct tta				1643
Phe Pro Val Asn Phe Arg Lys Phe Gly Asp Asn Met Lys Ala Leu	510	515	520	
gca ata ata ttt tta ttt gta agc ata agt ttt gca aac gaa aac ata				1691
Ala Ile Ile Phe Leu Phe Val Ser Ile Ser Phe Ala Asn Glu Asn Ile	525	530	535	
acc gac gct ttt caa ata cgc aat gca aac acc gga att cct ata aat				1739

Thr	Asp	Ala	Phe	Gln	Ile	Arg	Asn	Ala	Asn	Thr	Gly	Ile	Pro	Ile	Asn		
540						545					550						
ata	aag	cga	ttt	tca	ggg	cag	ttt	aat	tac	caa	aac	tg	ttt	tta	aat	1787	
Ile	Lys	Arg	Phe	Ser	Gly	Gln	Phe	Asn	Tyr	Gln	Asn	Trp	Phe	Leu	Asn		
555					560					565					570		
gat	tta	gga	gta	gat	cct	aag	ata	aaa	aaa	gta	gat	aaa	ttt	tca	aat	1835	
Asp	Leu	Gly	Val	Asp	Pro	Lys	Ile	Lys	Lys	Val	Asp	Lys	Phe	Ser	Asn		
				575						580					585		
tct	ttt	cct	ttt	gga	tac	gtg	caa	ttt	caa	gta	gca	gcc	gac	gta	aaa	1883	
Ser	Phe	Pro	Phe	Gly	Tyr	Val	Gln	Phe	Gln	Val	Ala	Ala	Asp	Val	Lys		
				590				595					600				
atg	tgc	ctt	cag	atc	gct	cct	agc	gga	ttt	tta	gca	cta	aaa	aac	tgc	1931	
Met	Cys	Leu	Gln	Ile	Ala	Pro	Ser	Gly	Phe	Leu	Ala	Leu	Lys	Asn	Cys		
		605					610					615					
aag	caa	gac	tac	gat	agc	gga	gag	ttt	gag	act	att	ttt	cag	atc	atc	1979	
Lys	Gln	Asp	Tyr	Asp	Ser	Gly	Glu	Phe	Glu	Thr	Ile	Phe	Gln	Ile	Ile		
	620					625					630						
cct	aca	agt	agt	gga	gct	atg	cag	cta	cga	tca	cta	ggt	cta	aaa	aca	2027	
Pro	Thr	Ser	Ser	Gly	Ala	Met	Gln	Leu	Arg	Ser	Leu	Val	Leu	Lys	Thr		
635					640					645					650		
aac	gag	tgc	tta	gga	aca	ttt	gaa	aat	cca	aac	gtg	ccg	atc	gaa	gat	2075	
Asn	Glu	Cys	Leu	Gly	Thr	Phe	Glu	Asn	Pro	Asn	Val	Pro	Ile	Glu	Asp		
				655					660					665			
aga	gta	gga	cta	gta	cgc	tgc	gtt	tta	gaa	ttt	ttt	gtc	gac	ata	gag	2123	
Arg	Val	Gly	Leu	Val	Arg	Cys	Val	Leu	Glu	Phe	Phe	Val	Asp	Ile	Glu		
				670				675					680				
cct	aaa	caa	ctt	ttt	gta	ttt	tca	ccg	ccg	ctt	agt	gaa	gct	aag	gta	2171	
Pro	Lys	Gln	Leu	Phe	Val	Phe	Ser	Pro	Pro	Leu	Ser	Glu	Ala	Lys	Val		
		685					690					695					
att	aga	taa														2180	
Ile	Arg																
	700																

<210> 52
 <211> 234
 <212> PRT
 <213> Campylobacter fetus

<400> 52

Met	Thr	Lys	Ile	Ile	Phe	Lys	His	Ile	Lys	Asn	Ser	Leu	Ile	Leu	Leu
1				5					10					15	

Phe	Cys	Ile	Ala	Leu	Phe	Ser	Ala	Cys	Ser	Ser	Lys	Thr	Thr	Asn	Val
			20					25					30		

Ser Thr Gln Lys Ile Asn Pro Leu Gly Ser Ile Phe Gly Lys Thr Asp
 35 40 45

Asp Pro Asp Pro Leu Asn Leu Gly Asp Phe Pro Thr Leu Leu Thr Ser
 50 55 60

Asn Phe Thr Asn Pro Met Pro Thr Arg Thr Pro Ser Pro Leu Lys Lys
 65 70 75 80

Val Asp Leu Pro Val Met Asn Ser Leu Thr His Gly Pro Met Phe Ser
 85 90 95

Ser Ala Phe Ser Lys Pro Asp Leu Asn Phe Lys Gln Pro Thr Ile Ser
 100 105 110

Leu Gln Gly Ile Pro Pro Asp Leu Phe Asp Arg Thr Ser Asp Phe Met
 115 120 125

Val Ile Met Gly Ala Asn Gly Val Val Ile Thr Ile Trp Tyr Thr Ser
 130 135 140

Pro Gly Asn Trp Leu Trp Gly Tyr Ser Leu Tyr Glu Ser Gly Asn Leu
 145 150 155 160

Gly Gly Tyr Arg Val Trp Arg Leu Ile Leu Leu Pro Asn Asn Glu Val
 165 170 175

Met Ile Val Asn Phe Asn Thr Arg Thr Thr Cys Ile Asn Thr Tyr Lys
 180 185 190

Asn Gly Val Ile His Ser Pro Cys Asn Lys Asp Asn Pro Phe Gln Lys
 195 200 205

Phe Thr Phe Arg Pro Met Thr Asn Gly Ala Val Gln Ile Tyr Asn Lys
 210 215 220

Ala Thr Asn Cys Val Leu Ala Asn Ala Cys
 225 230

<210> 53
 <211> 284
 <212> PRT
 <213> Campylobacter fetus

<400> 53

Met Val Phe Ala Pro Ala Ala Ala Ser Trp Lys Thr Ile Leu Leu Gly
 1 5 10 15

Val Lys Met Arg Asn Val Ile Met Ile Ile Phe Ile Ala Thr Leu Gly
 20 25 30

Phe Ala Lys Pro Glu Asp Tyr Lys Ile Ala Thr Trp Asn Leu Gln Gly
 35 40 45

Ser Ser Ala Ile Thr Glu Ser Lys Trp Asn Ile Ser Val Arg Gln Ile
 50 55 60

Ile Ser Gly Glu Asn Pro Ala Asp Ile Leu Ala Val Gln Glu Ala Gly
 65 70 75 80

Asn Leu Pro Gln Thr Ala Leu Pro Thr Gly Arg Ser Ile Asn Gln Gly
 85 90 95

Gly Thr Ile Val Thr Glu His Leu Trp Gln Leu Gly Ser Ile Ser Arg
 100 105 110

Pro Phe Gln Val Tyr Ile Tyr Tyr Ala Gln Ile Asp Thr Gly Ala Asn
 115 120 125

Arg Val Asn Leu Ala Ile Val Ser Arg Ile Lys Ala Asp Glu Ile Ile
 130 135 140

Ile Leu Pro Pro Pro Thr Val Ala Ser Arg Pro Leu Ile Gly Ile Arg
 145 150 155 160

Ile Gly Asn Asp Val Phe Phe Asn Ile His Ala Leu Ala Asn Gly Gly
 165 170 175

Val Asp Ala Pro Ala Ile Ile Asn Ser Ile Phe Asp Arg Phe Arg Asn
 180 185 190

Met Pro Asn Ile Thr Trp Met Ile Leu Gly Asp Phe Asn Arg Ser Pro
 195 200 205

Glu Ser Leu Arg Gly Thr Leu Gly Leu Glu Thr Arg Val Arg Val Thr
 210 215 220

Phe Leu Thr Pro Pro Ala Pro Thr Gln Arg Ser Gly Gly Thr Leu Asp
 225 230 235 240

Trp Ala Ile Val Gly Asn Ser Ala Gly Asp Leu Val Arg Thr Thr Leu
245 250 255

Val Ala Val Leu Met Leu Ala Asn Leu Arg Thr His Leu Val Ser Asp
260 265 270

His Phe Pro Val Asn Phe Arg Lys Phe Gly Asp Asn
275 280

<210> 54
<211> 182
<212> PRT
<213> Campylobacter fetus
<400> 54

Met Lys Ala Leu Ala Ile Ile Phe Leu Phe Val Ser Ile Ser Phe Ala
1 5 10 15

Asn Glu Asn Ile Thr Asp Ala Phe Gln Ile Arg Asn Ala Asn Thr Gly
20 25 30

Ile Pro Ile Asn Ile Lys Arg Phe Ser Gly Gln Phe Asn Tyr Gln Asn
35 40 45

Trp Phe Leu Asn Asp Leu Gly Val Asp Pro Lys Ile Lys Lys Val Asp
50 55 60

Lys Phe Ser Asn Ser Phe Pro Phe Gly Tyr Val Gln Phe Gln Val Ala
65 70 75 80

Ala Asp Val Lys Met Cys Leu Gln Ile Ala Pro Ser Gly Phe Leu Ala
85 90 95

Leu Lys Asn Cys Lys Gln Asp Tyr Asp Ser Gly Glu Phe Glu Thr Ile
100 105 110

Phe Gln Ile Ile Pro Thr Ser Ser Gly Ala Met Gln Leu Arg Ser Leu
115 120 125

Val Leu Lys Thr Asn Glu Cys Leu Gly Thr Phe Glu Asn Pro Asn Val
130 135 140

Pro Ile Glu Asp Arg Val Gly Leu Val Arg Cys Val Leu Glu Phe Phe
145 150 155 160

Val Asp Ile Glu Pro Lys Gln Leu Phe Val Phe Ser Pro Pro Leu Ser
165 170 175

Glu Ala Lys Val Ile Arg
180

<210> 55
<211> 29
<212> DNA
<213> Artificial

<220>
<223> an artificially synthesized primer sequence

<220>
<221> misc_feature
<222> (21)..(29)
<223> "n" indicates a, t, g, or ,c

<400> 55
gctttagca gtattgatgc nnnnnnnnn

29

<210> 56
<211> 20
<212> DNA
<213> Artificial

<220>
<223> an artificially synthesized primer sequence

<400> 56
gctttagca gtattgatgc

20

<210> 57
<211> 20
<212> DNA
<213> Artificial

<220>
<223> an artificially synthesized primer sequence

<400> 57
ctagtttcgg accattttcc

20

<210> 58
<211> 29
<212> DNA
<213> Artificial

<220>
<223> an artificially synthesized primer sequence

<220>
<221> misc_feature
<222> (21)..(29)
<223> "n" indicates a, t, g, or ,c

<400> 58
atacgcaatg caaacaccgg nnnnnnnnn

29

<210> 59
<211> 19
<212> DNA
<213> Artificial

<220>
<223> an artificially synthesized primer sequence

<400> 59
atacgcaatg aaacaccgg

19

<210> 60
<211> 21
<212> DNA
<213> Artificial

<220>
<223> an artificially synthesized primer sequence

<400> 60
taaaagcgat tttcagggca g

21

<210> 61
<211> 29
<212> DNA
<213> Artificial

<220>
<223> an artificially synthesized primer sequence

<220>
<221> misc_feature
<222> (21)..(29)
<223> "n" indicates a, t, g, or ,c

<400> 61
tgtcgacata gagcctaaac nnnnnnnnn

29

<210> 62
<211> 20
<212> DNA
<213> Artificial

<220>
<223> an artificially synthesized primer sequence

<400> 62
tgtcgacata gaggcctaaac 20

<210> 63
<211> 20
<212> DNA
<213> Artificial

<220>
<223> an artificially synthesized primer sequence

<400> 63
attttcaccg ccgcttagtg 20

<210> 64
<211> 34
<212> DNA
<213> Artificial

<220>
<223> an artificially synthesized primer sequence

<400> 64
gaaactgata cactaggata cgatccattc caaa 34

<210> 65
<211> 28
<212> DNA
<213> Artificial

<220>
<223> an artificially synthesized primer sequence

<400> 65
gaataatcag gtcgctttgc taatgaca 28

<210> 66
<211> 33
<212> DNA
<213> Artificial

<220>
<223> an artificially synthesized primer sequence

<400> 66
agcatgtctc atagatatgt actcaaaact tgg 33

<210> 67
<211> 32
<212> DNA
<213> Artificial

<220>

<223> an artificially synthesized primer sequence

<400> 67
agcctaagta tccataacgt cgtattcttt gc 32

<210> 68
<211> 20
<212> DNA
<213> Artificial

<220>
<223> an artificially synthesized primer sequence

<400> 68
aggacttgaa cctacttttc 20

<210> 69
<211> 20
<212> DNA
<213> Artificial

<220>
<223> an artificially synthesized primer sequence

<400> 69
aggtggagta gttaaaaacc 20

<210> 70
<211> 20
<212> DNA
<213> Artificial

<220>
<223> an artificially synthesized primer sequence

<400> 70
attgccaaagg ctaaaatctc 20

<210> 71
<211> 18
<212> DNA
<213> Artificial

<220>
<223> an artificially synthesized primer sequence

<400> 71
gataaagtct aaaactgc 18

<210> 72
<211> 20
<212> DNA
<213> Artificial

<220>
 <223> an artificially synthesized primer sequence
 <400> 72
 aacgacaaat gtaagcactc 20

<210> 73
 <211> 20
 <212> DNA
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<220>
 <223> an artificially synthesized primer sequence
 <400> 73
 tatattatgca agtcgtgcga 20

<210> 74
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 <212> DNA
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<220>
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 <400> 74
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<210> 75
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<220>
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 <400> 75
 aaggggtagc agctgttaa 19

<210> 76
 <211> 21
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 <213> Artificial

<220>
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 <400> 76
 taggggatat gcacgcaaaa g 21

<210> 77
 <211> 20
 <212> DNA
 <213> Artificial

<220>
<223> an artificially synthesized primer sequence

<400> 77
gcttaataca gttacgatag 20

<210> 78
<211> 20
<212> DNA
<213> Artificial

<220>
<223> an artificially synthesized primer sequence

<400> 78
aagcataagt ttgcaaacg 20

<210> 79
<211> 21
<212> DNA
<213> Artificial

<220>
<223> an artificially synthesized primer sequence

<400> 79
gtttggattt tcaaattgttc c 21